



## IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant: June *et al.*

Serial No.: 09/349,915

Filing Date: July 8, 1999

Title: Methods for Selectively Stimulating  
Proliferation of T-Cells

Art Unit: 1636

Examiner: Unassigned


Commissioner for Patents  
Washington, DC 20231

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**CERTIFICATION UNDER 37 C.F.R. § 1.10**

I hereby certify that the attached papers are being deposited with the United States Postal Service as "Express Mail Post Office to Addressee" Service under 37 C.F.R. § 1.10 on 17 May 2002 addressed to: **BOX SEQUENCE**, U.S. Patent and Trademark Office, 2011 South Clark Place, Customer Window, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

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Becky Johnson

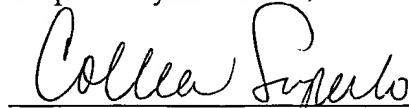
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**STATEMENT UNDER 37 C.F.R. § 1.821(f)**

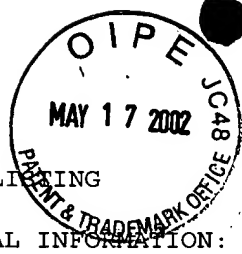
The substitute diskette enclosed herewith contains a computer readable form of the Sequence Listing for the above-referenced patent application. The information recorded in computer readable form on the diskette is identical to the substitute written Sequence Listing. The computer readable form of the Sequence Listing contained on this diskette is understood to comply with the requirements of § 1.821(f).

Dated: May 17, 2002

Respectfully submitted,

  
Colleen Superko  
Registration No. 39,850

Hale and Dorr LLP  
60 State Street  
Boston, MA 02481  
Tel: 617-526-6564  
Fax: 617-526-5000



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: June, Carl H., Thompson, Craig B., Nabel, Gary J.  
Gray, Gary S., Rennert, Paul D.
- (ii) TITLE OF INVENTION: Methods For Selectively Stimulating  
Proliferation Of T-Cells
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: HALE AND DORR LLP
  - (B) STREET: 60 State Street
  - (C) CITY: Boston
  - (D) STATE: Massachusetts
  - (E) COUNTRY: USA
  - (F) ZIP: 02109
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: 09/349,915
  - (B) FILING DATE: July 8, 1999
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/403,253
  - (B) FILING DATE: March 10, 1995
  - (A) APPLICATION NUMBER: US 08/253,964
  - (B) FILING DATE: 3 JUNE 1994
  - (A) APPLICATION NUMBER: US 08/073,223
  - (B) FILING DATE: 4 JUNE 1993
  - (A) APPLICATION NUMBER: US 08/200,947
  - (B) FILING DATE: 23 FEB 1994
  - (A) APPLICATION NUMBER: US 07/864,805
  - (B) FILING DATE: 7 APR 1992
  - (A) APPLICATION NUMBER: US 08/247,505
  - (B) FILING DATE: 23 MAY 1994
  - (A) APPLICATION NUMBER: US 07/864,866
  - (B) FILING DATE: 7 APR 1992
  - (A) APPLICATION NUMBER: US 08/218,155
  - (B) FILING DATE: 25 MAR 1994
  - (A) APPLICATION NUMBER: US 07/864,807
  - (B) FILING DATE: 7 APR 1992
  - (A) APPLICATION NUMBER: US 07/902,467
  - (B) FILING DATE: 16 JUNE 1992
  - (A) APPLICATION NUMBER: US 07/275,433
  - (B) FILING DATE: 23 NOV 1988
- (viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Mandragouras, Amy E.
- (B) REGISTRATION NUMBER: 36,207
- (C) REFERENCE/DOCKET NUMBER: RPI-002CP2

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (617) 227-7400
- (B) TELEFAX: (617) 742-4214

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapien
- (F) TISSUE TYPE: lymphoid
- (G) CELL TYPE: B cell
- (H) CELL LINE: Raji

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA in pCDM8 vector
- (B) CLONE: B7, Raji clone #13

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: 3

(ix) FEATURE:

- (A) NAME/KEY: Open reading frame (translated region)
- (B) LOCATION: 318 to 1181 bp
- (C) IDENTIFICATION METHOD: similarity to other pattern

(ix) FEATURE:

- (A) NAME/KEY: Alternate polyadenylation signal
- (B) LOCATION: 1474 to 1479 bp
- (C) IDENTIFICATION METHOD: similarity to other pattern

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: FREEMAN, GORDON J.  
FREEDMAN, ARNOLD S.  
SEGIL, JEFFREY M.

LEE, GRACE  
WHITMAN, JAMES F.  
NADLER, LEE M.

(B) TITLE: B7, A New Member Of The Ig Superfamily With  
Unique Expression On Activated And Neoplastic B Cells  
(C) JOURNAL: The Journal of Immunology  
(D) VOLUME: 143  
(E) ISSUE: 8  
(F) PAGES: 2714-2722  
(G) DATE: 15-OCT-1989  
(H) RELEVANT RESIDUES In SEQ ID NO:1: FROM 1 TO 1491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCAAAGAAAA	AGTGATTTGT	CATTGCTTTA	TAGACTGTAA	GAAGAGAACA	TCTCAGAAGT	60										
GGAGTCTTAC	CCTGAAATCA	AAGGATTTAA	AGAAAAAGTG	GAATTTTCT	TCAGCAAGCT	120										
GTGAAACTAA	ATCCACAACC	TTTGAGAGACC	CAGGAACACC	CTCCAATCTC	TGTGTGTTTT	180										
GTAAACATCA	CTGGAGGGTC	TTCTACGTGA	GCAATTGGAT	TGTCATCAGC	CCTGCCTGTT	240										
TTGCACCTGG	GAAGTGCCCT	GGTCTTACTT	GGGTCCAAAT	TGTTGGCTTT	CACTTTTGAC	300										
CCTAAGCATC	TGAAGCC	ATG	GGC	CAC	ACA	CGG	AGG	CAG	GGA	ACA	TCA	CCA	TCC	353		
				Met	Gly	His	Thr	Arg	Arg	Gln	Gly	Thr	Ser	Pro	Ser	
														-30	-25	
AAG	TGT	CCA	TAC	CTG	AAT	TTC	TTT	CAG	CTC	TTG	GTG	CTG	GCT	GGT	CTT	401
Lys	Cys	Pro	Tyr	Leu	Asn	Phe	Phe	Gln	Leu	Leu	Val	Leu	Ala	Gly	Leu	
		-20					-15					-10				
TCT	CAC	TTC	TGT	TCA	GGT	GTT	ATC	CAC	GTG	ACC	AAG	GAA	GTG	AAA	GAA	449
Ser	His	Phe	Cys	Ser	Gly	Val	Ile	His	Val	Thr	Lys	Glu	Val	Lys	Glu	
	-5					1				5					10	
GTG	GCA	ACG	CTG	TCC	TGT	GGT	CAC	AAT	GTT	TCT	GTT	GAA	GAG	CTG	GCA	497
Val	Ala	Thr	Leu	Ser	Cys	Gly	His	Asn	Val	Ser	Val	Glu	Glu	Leu	Ala	
				15					20					25		
CAA	ACT	CGC	ATC	TAC	TGG	CAA	AAG	GAG	AAG	AAA	ATG	GTG	CTG	ACT	ATG	545
Gln	Thr	Arg	Ile	Tyr	Trp	Gln	Lys	Glu	Lys	Lys	Met	Val	Leu	Thr	Met	
			30					35						40		
ATG	TCT	GGG	GAC	ATG	AAT	ATA	TGG	CCC	GAG	TAC	AAG	AAC	CGG	ACC	ATC	593
Met	Ser	Gly	Asp	Met	Asn	Ile	Trp	Pro	Glu	Tyr	Lys	Asn	Arg	Thr	Ile	
		45					50					55				
TTT	GAT	ATC	ACT	AAT	AAC	CTC	TCC	ATT	GTG	ATC	CTG	GCT	CTG	CGC	CCA	641
Phe	Asp	Ile	Thr	Asn	Asn	Leu	Ser	Ile	Val	Ile	Leu	Ala	Leu	Arg	Pro	

60	65	70	
TCT GAC GAG GGC ACA TAC GAG TGT GTT GTT CTG AAG TAT GAA AAA GAC Ser Asp Glu Gly Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp 75 80 85 90	689		
GCT TTC AAG CGG GAA CAC CTG GCT GAA GTG ACG TTA TCA GTC AAA GCT Ala Phe Lys Arg Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala 95 100 105	737		
GAC TTC CCT ACA CCT AGT ATA TCT GAC TTT GAA ATT CCA ACT TCT AAT Asp Phe Pro Thr Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn 110 115 120	785		
ATT AGA AGG ATA ATT TGC TCA ACC TCT GGA GGT TTT CCA GAG CCT CAC Ile Arg Arg Ile Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His 125 130 135	833		
CTC TCC TGG TTG GAA AAT GGA GAA GAA TTA AAT GCC ATC AAC ACA ACA Leu Ser Trp Leu Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr 140 145 150	881		
GTT TCC CAA GAT CCT GAA ACT GAG CTC TAT GCT GTT AGC AGC AAA CTG Val Ser Gln Asp Pro Glu Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu 155 160 165 170	929		
GAT TTC AAT ATG ACA ACC AAC CAC AGC TTC ATG TGT CTC ATC AAG TAT Asp Phe Asn Met Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys Tyr 175 180 185	977		
GGA CAT TTA AGA GTG AAT CAG ACC TTC AAC TGG AAT ACA ACC AAG CAA Gly His Leu Arg Val Asn Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln 190 195 200	1025		
GAG CAT TTT CCT GAT AAC CTG CTC CCA TCC TGG GCC ATT ACC TTA ATC Glu His Phe Pro Asp Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu Ile 205 210 215	1073		
TCA GTA AAT GGA ATT TTT GTG ATA TGC TGC CTG ACC TAC TGC TTT GCC Ser Val Asn Gly Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala 220 225 230	1121		
CCA AGA TGC AGA GAG AGA AGG AGG AAT GAG AGA TTG AGA AGG GAA AGT Pro Arg Cys Arg Glu Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser 235 240 245 250	1169		

GTA CGC CCT GTA TAACAGTGTC CGCAGAAGCA AGGGGCTGAA AAGATCTGAA 1221  
Val Arg Pro Val

GGTAGCCTCC GTCATCTCTT CTGGGATACA TGGATCGTGG GGATCATGAG GCATTCTTCC 1281

CTTAACAAAT TTAAGCTGTT TTACCCACTA CCTCACCTTC TTAAAAACCT CTTTCAGATT 1341

AAGCTGAACA GTTACAAGAT GGCTGGCATC CCTCTCCTTT CTCCCCATAT GCAATTTGCT 1401

TAATGTAACC TCTTCTTTTG CCATGTTTCC ATTCTGCCAT CTTGAATTGT CTTGTCAGCC 1461

AATTCATTAT CTATTAAACA CTAATTTGAG 1491

(3) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (A) DESCRIPTION: B cell activation antigen; natural ligand  
for CD28 T cell surface antigen; transmembrane protein

(ix) FEATURE:

- (A) NAME/KEY: signal sequence
- (B) LOCATION: -34 to -1
- (C) IDENTIFICATION METHOD: amino terminal sequencing of  
soluble protein
- (D) OTHER INFORMATION: hydrophobic

(ix) FEATURE:

- (A) NAME/KEY: extracellular domain
- (B) LOCATION: 1 to 208
- (C) IDENTIFICATION METHOD: similarity with known  
sequence

(ix) FEATURE:

- (A) NAME/KEY: transmembrane domain
- (B) LOCATION: 209 to 235
- (C) IDENTIFICATION METHOD: similarity with known  
sequence

(ix) FEATURE:

- (A) NAME/KEY: intracellular domain
- (B) LOCATION: 236 to 254
- (C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- (A) NAME/KEY: N-linked glycosylation
- (B) LOCATION: 19 to 21
- (C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- (A) NAME/KEY: N-linked glycosylation
- (B) LOCATION: 55 to 57
- (C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- (A) NAME/KEY: N-linked glycosylation
- (B) LOCATION: 64 to 66
- (C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- (A) NAME/KEY: N-linked glycosylation
- (B) LOCATION: 152 to 154
- (C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- (A) NAME/KEY: N-linked glycosylation
- (B) LOCATION: 173 to 175
- (C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- (A) NAME/KEY: N-linked glycosylation
- (B) LOCATION: 177 to 179
- (C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- (A) NAME/KEY: N-linked glycosylation
- (B) LOCATION: 192 to 194
- (C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- (A) NAME/KEY: N-linked glycosylation
- (B) LOCATION: 198 to 200
- (C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- (A) NAME/KEY: Ig V-set domain
- (B) LOCATION: 1 to 104
- (C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- (A) NAME/KEY: Ig C-set domain
- (B) LOCATION: 105 to 202
- (C) IDENTIFICATION METHOD: similarity with known sequence

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: FREEMAN, GORDON J.  
FREEDMAN, ARNOLD S.  
SEGIL, JEFFREY M.  
LEE, GRACE  
WHITMAN, JAMES F.  
NADLER, LEE M.
- (B) TITLE: B7, A New Member Of The Ig Superfamily With Unique Expression On Activated And Neoplastic B Cells
- (C) JOURNAL: The Journal of Immunology
- (D) VOLUME: 143
- (E) ISSUE: 8
- (F) PAGES: 2714-2722
- (G) DATE: 15-OCT-1989
- (H) RELEVANT RESIDUES IN SEQUENCE ID NO:2: From -26 to 262

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Gly	His	Thr	Arg	Arg	Gln	Gly	Thr	Ser	Pro	Ser	Lys	Cys	Pro	Tyr
				-30					-25					-20	
Leu	Asn	Phe	Phe	Gln	Leu	Leu	Val	Leu	Ala	Gly	Leu	Ser	His	Phe	Cys
		-15					-10						-5		
Ser	Gly	Val	Ile	His	Val	Thr	Lys	Glu	Val	Lys	Glu	Val	Ala	Thr	Leu





(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 107..1093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CACAGGGTGA AAGCTTTGCT TCTCTGCTGC TGTAACAGGG ACTAGCACAG ACACACGGAT	60
 GAGTGGGGTTC ATTTCCAGAT ATTAGGTCAC AGCAGAAGCA GCCAAA ATG GAT CCC	115
<div style="text-align: right;">Met Asp Pro</div>	
<div style="text-align: center;">1</div>	
 CAG TGC ACT ATG GGA CTG AGT AAC ATT CTC TTT GTG ATG GCC TTC CTG	163
Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu	
<div style="display: flex; justify-content: space-between;"><div>5</div><div>10</div><div>15</div></div>	
 CTC TCT GGT GCT GCT CCT CTG AAG ATT CAA GCT TAT TTC AAT GAG ACT	211
Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr	
<div style="display: flex; justify-content: space-between;"><div>20</div><div>25</div><div>30</div><div>35</div></div>	
 GCA GAC CTG CCA TGC CAA TTT GCA AAC TCT CAA AAC CAA AGC CTG AGT	259
Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser	
<div style="display: flex; justify-content: space-between;"><div>40</div><div>45</div><div>50</div></div>	
 GAG CTA GTA GTA TTT TGG CAG GAC CAG GAA AAC TTG GTT CTG AAT GAG	307
Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu	
<div style="display: flex; justify-content: space-between;"><div>55</div><div>60</div><div>65</div></div>	
 GTA TAC TTA GGC AAA GAG AAA TTT GAC AGT GTT CAT TCC AAG TAT ATG	355
Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met	
<div style="display: flex; justify-content: space-between;"><div>70</div><div>75</div><div>80</div></div>	
 GGC CGC ACA AGT TTT GAT TCG GAC AGT TGG ACC CTG AGA CTT CAC AAT	403
Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn	
<div style="display: flex; justify-content: space-between;"><div>85</div><div>90</div><div>95</div></div>	
 CTT CAG ATC AAG GAC AAG GGC TTG TAT CAA TGT ATC ATC CAT CAC AAA	451
Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys	
<div style="display: flex; justify-content: space-between;"><div>100</div><div>105</div><div>110</div><div>115</div></div>	
 AAG CCC ACA GGA ATG ATT CGC ATC CAC CAG ATG AAT TCT GAA CTG TCA	499
Lys Pro Thr Gly Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser	
<div style="display: flex; justify-content: space-between;"><div>120</div><div>125</div><div>130</div></div>	
 GTG CTT GCT AAC TTC AGT CAA CCT GAA ATA GTA CCA ATT TCT AAT ATA	547
Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile	
<div style="display: flex; justify-content: space-between;"><div>135</div><div>140</div><div>145</div></div>	
 ACA GAA AAT GTG TAC ATA AAT TTG ACC TGC TCA TCT ATA CAC GGT TAC	595
Thr Glu Asn Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr	
<div style="display: flex; justify-content: space-between;"><div>150</div><div>155</div><div>160</div></div>	
 CCA GAA CCT AAG AAG ATG AGT GTT TTG CTA AGA ACC AAG AAT TCA ACT	643

Pro	Glu	Pro	Lys	Lys	Met	Ser	Val	Leu	Leu	Arg	Thr	Lys	Asn	Ser	Thr	
165						170					175					
ATC	GAG	TAT	GAT	GGT	ATT	ATG	CAG	AAA	TCT	CAA	GAT	AAT	GTC	ACA	GAA	691
Ile	Glu	Tyr	Asp	Gly	Ile	Met	Gln	Lys	Ser	Gln	Asp	Asn	Val	Thr	Glu	
180					185					190					195	
CTG	TAC	GAC	GTT	TCC	ATC	AGC	TTG	TCT	GTT	TCA	TTC	CCT	GAT	GTT	ACG	739
Leu	Tyr	Asp	Val	Ser	Ile	Ser	Leu	Ser	Val	Ser	Phe	Pro	Asp	Val	Thr	
				200					205					210		
AGC	AAT	ATG	ACC	ATC	TTC	TGT	ATT	CTG	GAA	ACT	GAC	AAG	ACG	CGG	CTT	787
Ser	Asn	Met	Thr	Ile	Phe	Cys	Ile	Leu	Glu	Thr	Asp	Lys	Thr	Arg	Leu	
			215					220					225			
TTA	TCT	TCA	CCT	TTC	TCT	ATA	GAG	CTT	GAG	GAC	CCT	CAG	CCT	CCC	CCA	835
Leu	Ser	Ser	Pro	Phe	Ser	Ile	Glu	Leu	Glu	Asp	Pro	Gln	Pro	Pro	Pro	
			230				235						240			
GAC	CAC	ATT	CCT	TGG	ATT	ACA	GCT	GTA	CTT	CCA	ACA	GTT	ATT	ATA	TGT	883
Asp	His	Ile	Pro	Trp	Ile	Thr	Ala	Val	Leu	Pro	Thr	Val	Ile	Ile	Cys	
	245					250					255					
GTG	ATG	GTT	TTC	TGT	CTA	ATT	CTA	TGG	AAA	TGG	AAG	AAG	AAG	AAG	CGG	931
Val	Met	Val	Phe	Cys	Leu	Ile	Leu	Trp	Lys	Trp	Lys	Lys	Lys	Lys	Arg	
260					265				270						275	
CCT	CGC	AAC	TCT	TAT	AAA	TGT	GGA	ACC	AAC	ACA	ATG	GAG	AGG	GAA	GAG	979
Pro	Arg	Asn	Ser	Tyr	Lys	Cys	Gly	Thr	Asn	Thr	Met	Glu	Arg	Glu	Glu	
				280					285					290		
AGT	GAA	CAG	ACC	AAG	AAA	AGA	GAA	AAA	ATC	CAT	ATA	CCT	GAA	AGA	TCT	1027
Ser	Glu	Gln	Thr	Lys	Lys	Arg	Glu	Lys	Ile	His	Ile	Pro	Glu	Arg	Ser	
			295					300					305			
GAT	GAA	GCC	CAG	CGT	GTT	TTT	AAA	AGT	TCG	AAG	ACA	TCT	TCA	TGC	GAC	1075
Asp	Glu	Ala	Gln	Arg	Val	Phe	Lys	Ser	Ser	Lys	Thr	Ser	Ser	Cys	Asp	
		310					315					320				
AAA	AGT	GAT	ACA	TGT	TTT	TAATTAAAGA	GTAAAGCCCA	AAAAAAA								1120
Lys	Ser	Asp	Thr	Cys	Phe											
						325										

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Asp	Pro	Gln	Cys	Thr	Met	Gly	Leu	Ser	Asn	Ile	Leu	Phe	Val	Met	
1				5				10					15			

Ala	Phe	Leu	Leu	Ser	Gly	Ala	Ala	Pro	Leu	Lys	Ile	Gln	Ala	Tyr	Phe		
		20						25					30				
Asn	Glu	Thr	Ala	Asp	Leu	Pro	Cys	Gln	Phe	Ala	Asn	Ser	Gln	Asn	Gln		
		35					40					45					
Ser	Leu	Ser	Glu	Leu	Val	Val	Phe	Trp	Gln	Asp	Gln	Glu	Asn	Leu	Val		
	50					55					60						
Leu	Asn	Glu	Val	Tyr	Leu	Gly	Lys	Glu	Lys	Phe	Asp	Ser	Val	His	Ser		
65					70					75					80		
Lys	Tyr	Met	Gly	Arg	Thr	Ser	Phe	Asp	Ser	Asp	Ser	Trp	Thr	Leu	Arg		
				85					90					95			
Leu	His	Asn	Leu	Gln	Ile	Lys	Asp	Lys	Gly	Leu	Tyr	Gln	Cys	Ile	Ile		
		100						105					110				
His	His	Lys	Lys	Pro	Thr	Gly	Met	Ile	Arg	Ile	His	Gln	Met	Asn	Ser		
		115					120					125					
Glu	Leu	Ser	Val	Leu	Ala	Asn	Phe	Ser	Gln	Pro	Glu	Ile	Val	Pro	Ile		
	130					135					140						
Ser	Asn	Ile	Thr	Glu	Asn	Val	Tyr	Ile	Asn	Leu	Thr	Cys	Ser	Ser	Ile		
145					150					155					160		
His	Gly	Tyr	Pro	Glu	Pro	Lys	Lys	Met	Ser	Val	Leu	Leu	Arg	Thr	Lys		
				165					170					175			
Asn	Ser	Thr	Ile	Glu	Tyr	Asp	Gly	Ile	Met	Gln	Lys	Ser	Gln	Asp	Asn		
		180						185					190				
Val	Thr	Glu	Leu	Tyr	Asp	Val	Ser	Ile	Ser	Leu	Ser	Val	Ser	Phe	Pro		
	195						200					205					
Asp	Val	Thr	Ser	Asn	Met	Thr	Ile	Phe	Cys	Ile	Leu	Glu	Thr	Asp	Lys		
	210					215					220						
Thr	Arg	Leu	Leu	Ser	Ser	Pro	Phe	Ser	Ile	Glu	Leu	Glu	Asp	Pro	Gln		
225				230						235					240		
Pro	Pro	Pro	Asp	His	Ile	Pro	Trp	Ile	Thr	Ala	Val	Leu	Pro	Thr	Val		
				245					250					255			
Ile	Ile	Cys	Val	Met	Val	Phe	Cys	Leu	Ile	Leu	Trp	Lys	Trp	Lys	Lys		
		260						265					270				
Lys	Lys	Arg	Pro	Arg	Asn	Ser	Tyr	Lys	Cys	Gly	Thr	Asn	Thr	Met	Glu		
		275					280					285					
Arg	Glu	Glu	Ser	Glu	Gln	Thr	Lys	Lys	Arg	Glu	Lys	Ile	His	Ile	Pro		
	290					295					300						
Glu	Arg	Ser	Asp	Glu	Ala	Gln	Arg	Val	Phe	Lys	Ser	Ser	Lys	Thr	Ser		

305

310

315

320

Ser Cys Asp Lys Ser Asp Thr Cys Phe  
325

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label=Xaa is any amino acid

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /label=Xaa is any amino acid

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /label=Xaa is any amino acid

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /label=Xaa is any amino acid

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 8
- (D) OTHER INFORMATION: /label=Xaa is Asp or Glu

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /label=Xaa is any amino acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Xaa Gly Xaa Trp Leu Xaa Xaa Xaa Xaa  
5

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Pro Val Lys Gly Gly Thr Lys Cys Ile Lys Tyr Leu Leu Phe Gly Phe  
                    5                    10                    15

Asn Phe Ile Phe Trp Leu Ala Gly Ile Ala Val Leu Ala Ile Gly Leu  
          20                    25                    30

Trp Leu Arg Phe Asp Ser Gln Thr Lys Ser Ile Phe Glu Gln Glu Thr  
      35                    40                    45

Asn Asn Asn Asn Ser Ser Phe Tyr Thr Gly Val Tyr Ile Leu Ile Gly  
      50                    55                    60

Ala Gly Ala Leu Met Met Leu Val Gly Phe Leu Gly Cys Cys Gly Ala  
      65                    70                    75                    80

Val Gln Glu Ser Gln Cys Met Leu Gly Leu Phe Phe Gly Phe Leu Leu  
          85                    90                    95

Val Ile Phe Ala Ile Glu Ile Ala Ala Ala Ile Trp Gly Tyr Ser His  
      100                    105                    110

Lys Asp Glu Val Ile Lys Glu Val Gln Glu Phe Tyr Lys Asp Thr Tyr  
      115                    120                    125

Asn Lys Leu Lys Thr Lys Asp Glu Pro Gln Arg Glu Thr Leu Lys Ala  
      130                    135                    140

Ile His Tyr Ala Leu Asn Cys Cys Gly Leu Ala Gly Gly Val Glu Gln  
      145                    150                    155                    160

Phe Ile Ser Asp Ile Cys Pro Lys Lys Asp Val Leu Glu Thr Phe Thr  
          165                    170                    175

Val Lys Ser Cys Pro Asp Ala Ile Lys Glu Val Phe Asp Asn Lys Phe  
      180                    185                    190

His Ile Ile Gly Ala Val Gly Ile Gly Ile Ala Val Val Met Ile Phe  
      195                    200                    205

Gly Met Ile Phe Ser Met Ile Leu Cys Cys Ala Ile Arg Arg Asn Arg  
      210                    215                    220

Glu Met Val  
225

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 7 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gly Leu Trp Leu Arg Phe Asp  
1 5

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

His Gln Phe Cys Asp His Trp Gly Cys Trp Leu Leu Arg Glu Thr His  
1 5 10 15  
Ile Phe Thr Pro  
20

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Leu Arg Leu Val Leu Glu Asp Pro Gly Ile Trp Leu Arg Pro Asp Tyr  
1 5 10 15  
Phe Phe Pro Ala  
20

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gly Cys Trp Leu Arg Glu  
1 5

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Gly Ile Trp Leu Arg Pro Asp  
1 5

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: 2  
(D) OTHER INFORMATION: /label=Xaa is any amino acid

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: 5  
(D) OTHER INFORMATION: /label=Xaa is any amino acid

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: 6  
(D) OTHER INFORMATION: /label=Xaa is Asp or Glu

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Gly Xaa Trp Leu Xaa Xaa  
1 5

(2) INFORMATION FOR SEQ ID NO:13:



- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CTTTAGAGCA CA

12

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTCTAAAG

8